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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/305,390

DATE: 05/18/1999
TIME: 10:05:15

Input Set: I305390.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Yamamoto, Hiroaki
2  <120> TITLE OF INVENTION: METHOD FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUT
3  ACID ESTER
4  <130> FILE REFERENCE: 06501/030001
5  <140> CURRENT APPLICATION NUMBER: US/09/305,390
6  <141> CURRENT FILING DATE: 1999-05-05
7  <150> EARLIER APPLICATION NUMBER: JP 1998-126507
8  <151> EARLIER FILING DATE: 1998-10-21
9  <150> EARLIER APPLICATION NUMBER: JP 1998-300178
10 <151> EARLIER FILING DATE: 1998-10-21
11 <160> NUMBER OF SEQ ID NOS: 18
12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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14 <211> LENGTH: 244
15 <212> TYPE: PRT
16 <213> ORGANISM: Escherichia coli
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20 Ile Gly Arg Ala Ile Ala Glu Thr Leu Ala Ala Arg Gly Ala Lys Val
21      20          25          30
22 Ile Gly Thr Ala Thr Ser Glu Asn Gly Ala Gln Ala Ile Ser Asp Tyr
23      35          40          45
24 Leu Gly Ala Asn Gly Lys Gly Leu Met Leu Asn Val Thr Asp Pro Ala
25      50          55          60
26 Ser Ile Glu Ser Val Leu Glu Lys Ile Arg Ala Glu Phe Gly Glu Val
27      65          70          75          80
28 Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Asn Leu Leu Met
29      85          90          95
30 Arg Met Lys Asp Glu Glu Trp Asn Asp Ile Ile Glu Thr Asn Leu Ser
31      100         105         110
32 Ser Val Phe Arg Leu Ser Lys Ala Val Met Arg Ala Met Met Lys Lys
33      115         120         125
34 Arg His Gly Arg Ile Ile Thr Ile Gly Ser Val Val Gly Thr Met Gly
35      130         135         140
36 Asn Gly Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala Gly Leu Ile Gly
37      145         150         155         160
38 Phe Ser Lys Ser Leu Ala Arg Glu Val Ala Ser Arg Gly Ile Thr Val
39      165         170         175
40 Asn Val Val Ala Pro Gly Phe Ile Glu Thr Asp Met Thr Arg Ala Leu
41      180         185         190
42 Ser Asp Asp Gln Arg Ala Gly Ile Leu Ala Gln Val Pro Ala Gly Arg
43      195         200         205
44 Leu Gly Gly Ala Gln Glu Ile Ala Asn Ala Val Ala Phe Leu Ala Ser

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45          210          215          220
46      Asp Glu Ala Ala Tyr Ile Thr Gly Glu Thr Leu His Val Asn Gly Gly
47          225          230          235          240
48      Met Tyr Met Val
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50      <211> LENGTH: 735
51      <212> TYPE: DNA
52      <213> ORGANISM: Escherichia coli
53      <220> FEATURE:
54      <221> NAME/KEY: CDS
55      <222> LOCATION: (1)...(732)
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58      Met Asn Phe Glu Gly Lys Ile Ala Leu Val Thr Gly Ala Ser Arg Gly
59      1          5          10          15
60      att ggc cgc gca att gct gaa acg ctc gca gcc cgt ggc gcg aaa gtt      96
61      Ile Gly Arg Ala Ile Ala Glu Thr Leu Ala Ala Arg Gly Ala Lys Val
62          20          25          30
63      att ggc act gcg acc agt gaa aat ggc gct cag gcg atc agt gat tat      144
64      Ile Gly Thr Ala Thr Ser Glu Asn Gly Ala Gln Ala Ile Ser Asp Tyr
65          35          40          45
66      tta ggt gcc aac ggc aaa ggt ctg atg ttg aat gtg acc gac ccg gca      192
67      Leu Gly Ala Asn Gly Lys Gly Leu Met Leu Asn Val Thr Asp Pro Ala
68          50          55          60
69      tct atc gaa tct gtt ctg gaa aaa att cgc gca gaa ttt ggt gaa gtg      240
70      Ser Ile Glu Ser Val Leu Glu Lys Ile Arg Ala Glu Phe Gly Glu Val
71      65          70          75          80
72      gat atc ctg gtc aat aat gcc ggt atc act cgt gat aac ctg tta atg      288
73      Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Asn Leu Leu Met
74          85          90          95
75      cga atg aaa gat gaa gag tgg aac gat att atc gaa acc aac ctt tca      336
76      Arg Met Lys Asp Glu Glu Trp Asn Asp Ile Ile Glu Thr Asn Leu Ser
77          100          105          110
78      tct gtt ttc cgt ctg tca aaa gcg gta atg cgc gct atg atg aaa aag      384
79      Ser Val Phe Arg Leu Ser Lys Ala Val Met Arg Ala Met Met Lys Lys
80          115          120          125
81      cgt cat ggt cgt att atc act atc ggt tct gtg gtt ggt acc atg gga      432
82      Arg His Gly Arg Ile Ile Thr Ile Gly Ser Val Val Gly Thr Met Gly
83          130          135          140
84      aat ggc ggt cag gcc aac tac gct gcg gcg aaa gcg ggc ttg atc ggc      480
85      Asn Gly Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala Gly Leu Ile Gly
86          145          150          155          160
87      ttc agt aaa tca ctg gcg cgc gaa gtt gcg tca cgc ggt att act gta      528
88      Phe Ser Lys Ser Leu Ala Arg Glu Val Ala Ser Arg Gly Ile Thr Val
89          165          170          175
90      aac gtt gtt gct ccg ggc ttt att gaa acg gac atg aca cgt gcg ctg      576
91      Asn Val Val Ala Pro Gly Phe Ile Glu Thr Asp Met Thr Arg Ala Leu
92          180          185          190
93      agc gat gac cag cgt gcg ggt atc ctg gcg cag gtt cct gcg ggt cgc      624
94      Ser Asp Asp Gln Arg Ala Gly Ile Leu Ala Gln Val Pro Ala Gly Arg

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95          195          200          205
96      ctc ggc ggc gca cag gaa atc gcc aac gcg gtt gca ttc ctg gca tcc      672
97      Leu Gly Gly Ala Gln Glu Ile Ala Asn Ala Val Ala Phe Leu Ala Ser
98          210          215          220
99      gac gaa gca gct tac atc acg ggt gaa act ttg cat gtg aac ggc ggg      720
100     Asp Glu Ala Ala Tyr Ile Thr Gly Glu Thr Leu His Val Asn Gly Gly
101     225          230          235          240
102     atg tac atg gtc tga      735
103     Met Tyr Met Val
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105     <211> LENGTH: 36
106     <212> TYPE: DNA
107     <213> ORGANISM: Artificial Sequence
108     <220> FEATURE:
109     <223> OTHER INFORMATION: Artificially synthesized primer sequence
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113     <211> LENGTH: 32
114     <212> TYPE: DNA
115     <213> ORGANISM: Artificial Sequence
116     <220> FEATURE:
117     <223> OTHER INFORMATION: Artificially synthesized primer sequence
118     <400> SEQUENCE: 4
119         tgcctcgagt tatcagacca tgtacatccc gc      32
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121     <211> LENGTH: 248
122     <212> TYPE: PRT
123     <213> ORGANISM: Bacillus subtilis
124     <400> SEQUENCE: 5
125     Met Asp Met Leu Asn Asp Lys Thr Ala Ile Val Thr Gly Ala Ser Arg
126         1          5          10          15
127     Gly Ile Gly Arg Ser Ile Ala Leu Ala Leu Ala Lys Ser Gly Ala Asn
128         20          25          30
129     Val Val Val Asn Tyr Ser Gly Asn Glu Ala Lys Ala Asn Glu Val Val
130         35          40          45
131     Asp Glu Ile Lys Ser Met Gly Arg Lys Ala Ile Ala Val Lys Ala Asp
132         50          55          60
133     Val Ser Asn Pro Glu Asp Val Gln Asn Met Ile Lys Glu Thr Leu Ser
134         65          70          75          80
135     Val Phe Ser Thr Ile Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg
136         85          90          95
137     Asp Asn Leu Ile Met Arg Met Lys Glu Asp Glu Trp Asp Asp Val Ile
138         100         105         110
139     Asn Ile Asn Leu Lys Gly Val Phe Asn Cys Thr Lys Ala Val Thr Arg
140         115         120         125
141     Gln Met Met Lys Gln Arg Ser Gly Arg Ile Ile Asn Val Ser Ser Ile
142         130         135         140
143     Val Gly Val Ser Gly Asn Pro Gly Gln Ala Asn Tyr Val Ala Ala Lys
144         145         150         155         160

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145      Ala Gly Val Ile Gly Leu Thr Lys Ser Ser Ala Lys Glu Leu Ala Ser
146              165              170              175
147      Arg Asn Ile Thr Val Asn Ala Ile Ala Pro Gly Phe Ile Ser Thr Asp
148              180              185              190
149      Met Thr Asp Lys Leu Ala Lys Asp Val Gln Asp Glu Met Leu Lys Gln
150              195              200              205
151      Ile Pro Leu Ala Arg Phe Gly Glu Pro Ser Asp Val Ser Ser Val Val
152              210              215              220
153      Thr Phe Leu Ala Ser Glu Gly Ala Arg Tyr Met Thr Gly Gln Thr Leu
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155      His Ile Asp Gly Gly Met Val Met
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158      <211> LENGTH: 747
159      <212> TYPE: DNA
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166      Met Asp Met Leu Asn Asp Lys Thr Ala Ile Val Thr Gly Ala Ser Arg
167      1              5              10              15
168      gga atc ggc cgc tca atc gcc ctt gct ctg gca aaa agc gga gca aat      96
169      Gly Ile Gly Arg Ser Ile Ala Leu Ala Leu Ala Lys Ser Gly Ala Asn
170              20              25              30
171      gtt gtc gtg aac tac tcc ggc aat gaa gcg aaa gca aat gaa gtg gta      144
172      Val Val Val Asn Tyr Ser Gly Asn Glu Ala Lys Ala Asn Glu Val Val
173              35              40              45
174      gat gaa atc aaa tca atg ggc aga aaa gca att gct gta aaa gcg gat      192
175      Asp Glu Ile Lys Ser Met Gly Arg Lys Ala Ile Ala Val Lys Ala Asp
176      50              55              60
177      gta tca aat ccc gaa gat gta caa aac atg ata aaa gaa aca ttg tct      240
178      Val Ser Asn Pro Glu Asp Val Gln Asn Met Ile Lys Glu Thr Leu Ser
179      65              70              75              80
180      gtt ttt tct acg att gac att ctg gtt aat aat gcg gga att aca aga      288
181      Val Phe Ser Thr Ile Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg
182              85              90              95
183      gac aat ctc atc atg aga atg aaa gaa gac gaa tgg gat gac gtc att      336
184      Asp Asn Leu Ile Met Arg Met Lys Glu Asp Glu Trp Asp Asp Val Ile
185              100              105              110
186      aac att aac ctg aag ggt gtt ttc aac tgc aca aaa gct gtt aca aga      384
187      Asn Ile Asn Leu Lys Gly Val Phe Asn Cys Thr Lys Ala Val Thr Arg
188              115              120              125
189      caa atg atg aaa cag cgt tca ggc cgc att att aac gta tcg tct atc      432
190      Gln Met Met Lys Gln Arg Ser Gly Arg Ile Ile Asn Val Ser Ser Ile
191      130              135              140
192      gtc ggc gtc agc gga aac cct gga caa gcc aac tac gtg gct gca aaa      480
193      Val Gly Val Ser Gly Asn Pro Gly Gln Ala Asn Tyr Val Ala Ala Lys
194      145              150              155              160

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195      gcc ggc gtc atc ggt tta acc aaa tct tct gct aaa gag ctc gcc agc      528
196      Ala Gly Val Ile Gly Leu Thr Lys Ser Ser Ala Lys Glu Leu Ala Ser
197      165      170      175
198      cga aat att acg gta aac gca ata gcg cca gga ttt atc tca act gat      576
199      Arg Asn Ile Thr Val Asn Ala Ile Ala Pro Gly Phe Ile Ser Thr Asp
200      180      185      190
201      atg aca gat aaa ctt gca aaa gac gtt caa gac gaa atg ctg aaa caa      624
202      Met Thr Asp Lys Leu Ala Lys Asp Val Gln Asp Glu Met Leu Lys Gln
203      195      200      205
204      att ccg ctc gcg cgc ttt ggt gaa cct agc gat gtc agc agt gtt gtc      672
205      Ile Pro Leu Ala Arg Phe Gly Glu Pro Ser Asp Val Ser Ser Val Val
206      210      215      220
207      acg ttc cta gct tca gag gga gct cgt tat atg aca ggc caa acg ctt      720
208      Thr Phe Leu Ala Ser Glu Gly Ala Arg Tyr Met Thr Gly Gln Thr Leu
209      225      230      235      240
210      cat att gac ggc gga atg gtg atg taa      747
211      His Ile Asp Gly Gly Met Val Met
212      245
213      <210> SEQ ID NO 7
214      <211> LENGTH: 33
215      <212> TYPE: DNA
216      <213> ORGANISM: Artificial Sequence
217      <220> FEATURE:
218      <223> OTHER INFORMATION: Artificially synthesized primer sequence
219      <400> SEQUENCE: 7
220      ggaccatgga tatgcttaat gataaaacgg cta      33
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222      <211> LENGTH: 34
223      <212> TYPE: DNA
224      <213> ORGANISM: Artificial Sequence
225      <220> FEATURE:
226      <223> OTHER INFORMATION: Artificially synthesized primer sequence
227      <400> SEQUENCE: 8
228      gagaagcttc tcgagttaca tcaccattcc gccg      34
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230      <211> LENGTH: 246
231      <212> TYPE: PRT
232      <213> ORGANISM: Ralstonia eutropha
233      <400> SEQUENCE: 9
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235      1      5      10      15
236      Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
237      20      25      30
238      Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
239      35      40      45
240      Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
241      50      55      60
242      Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
243      65      70      75      80
244      Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
